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RAW SEQUENCE LISTING

DATE: 09/14/2001

PATENT APPLICATION: US/09/835,694

TIME: 11:06:23

Input Set : A:\18972PCA.txt

Output Set: N:\CRF3\09142001\I835694.raw

SEQUENCE LISTING

C--> 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: DONNELLY, JOHN J.
6 DWARKI, VARAVANI J.
7 LIU, MARGARET A.
8 MONTGOMERY, DONNA L.
9 PARKER, SUEZANNE E.
10 SHIVER, JOHN W.
11 ULMER, JEFFREY B.

ENTERED

C--> 13 (ii) TITLE OF INVENTION: NUCLEIC ACID PHARMACEUTICALS - INFLUENZA MATRIX

15 (iii) NUMBER OF SEQUENCES: 64

17 (iv) CORRESPONDENCE ADDRESS:

18 (A) ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
19 (B) STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
20 (C) CITY: RAHWAY
21 (D) STATE: NJ
22 (E) COUNTRY: USA
23 (F) ZIP: 07065-0907

25 (v) COMPUTER READABLE FORM:

26 (A) MEDIUM TYPE: Diskette
27 (B) COMPUTER: IBM Compatible
28 (C) OPERATING SYSTEM: DOS
29 (D) SOFTWARE: FastSEQ Version 1.5

31 (vi) CURRENT APPLICATION DATA:

C--> 32 (A) APPLICATION NUMBER: US/09/835,694

C--> 33 (B) FILING DATE: 16-Apr-2001

34 (C) CLASSIFICATION:

48 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: 08/461 68
38 (B) FILING DATE: 05-June-1995
41 (A) APPLICATION NUMBER: PCT/US94/02751
42 (B) FILING DATE: 14-March-1994
45 (A) APPLICATION NUMBER: 08/089,985
46 (B) FILING DATE: 08-July-1993
49 (A) APPLICATION NUMBER: 08/032,383
50 (B) FILING DATE: 18-March-1993 OK

52 (viii) ATTORNEY/AGENT INFORMATION:

53 (A) NAME: HAND, J. MARK
54 (B) REGISTRATION NUMBER: 36,545
55 (C) REFERENCE/DOCKET NUMBER: 18972PCA

57 (ix) TELECOMMUNICATION INFORMATION:

58 (A) TELEPHONE: 732-594-3905
59 (B) TELEFAX: 732-594-4720
60 (C) TELEX:

63 (2) INFORMATION FOR SEQ ID NO: 1:

65 (i) SEQUENCE CHARACTERISTICS:

66 (A) LENGTH: 18 base pairs

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67          (B) TYPE: nucleic acid
68          (C) STRANDEDNESS: single
69          (D) TOPOLOGY: linear
71      (ii) MOLECULE TYPE: cDNA
72      (iii) HYPOTHETICAL: NO
C--> 73      (iv) ANTI-SENSE: NO
W--> 74      (v) FRAGMENT TYPE:
75      (vi) ORIGINAL SOURCE:
77      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
79  GTGTGCACCT CAAGCTGG                                     18
81  (2) INFORMATION FOR SEQ ID NO: 2:
83      (i) SEQUENCE CHARACTERISTICS:
84          (A) LENGTH: 23 base pairs
85          (B) TYPE: nucleic acid
86          (C) STRANDEDNESS: single
87          (D) TOPOLOGY: linear
89      (ii) MOLECULE TYPE: cDNA
90      (iii) HYPOTHETICAL: NO
C--> 91      (iv) ANTI-SENSE: NO
W--> 92      (v) FRAGMENT TYPE:
93      (vi) ORIGINAL SOURCE:
95      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
97  CCCTTTGAGA ATGTTGCACA TTC                               23
99  (2) INFORMATION FOR SEQ ID NO: 3:
101      (i) SEQUENCE CHARACTERISTICS:
102          (A) LENGTH: 33 base pairs
103          (B) TYPE: nucleic acid
104          (C) STRANDEDNESS: single
105          (D) TOPOLOGY: linear
107      (ii) MOLECULE TYPE: cDNA
108      (iii) HYPOTHETICAL: NO
C--> 109      (iv) ANTI-SENSE: NO
W--> 110      (v) FRAGMENT TYPE:
111      (vi) ORIGINAL SOURCE:
113      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
115  GGTACAAGAT CTACCATGCT TCTAACCGAG GTC                 33
117  (2) INFORMATION FOR SEQ ID NO: 4:
119      (i) SEQUENCE CHARACTERISTICS:
120          (A) LENGTH: 36 base pairs
121          (B) TYPE: nucleic acid
122          (C) STRANDEDNESS: single
123          (D) TOPOLOGY: linear
125      (ii) MOLECULE TYPE: cDNA
126      (iii) HYPOTHETICAL: NO
C--> 127      (iv) ANTI-SENSE: YES
W--> 128      (v) FRAGMENT TYPE:
129      (vi) ORIGINAL SOURCE:
131      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
133  CCACATAGAT CTTCACTTGA ACCGTTGCAT CTGCAC             36

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135 (2) INFORMATION FOR SEQ ID NO: 5:
137     (i) SEQUENCE CHARACTERISTICS:
138         (A) LENGTH: 23 base pairs
139         (B) TYPE: nucleic acid
140         (C) STRANDEDNESS: single
141         (D) TOPOLOGY: linear
143     (ii) MOLECULE TYPE: cDNA
144     (iii) HYPOTHETICAL: NO
C--> 145     (iv) ANTI-SENSE: NO
W--> 146     (v) FRAGMENT TYPE:
147         (vi) ORIGINAL SOURCE:
149     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
151 CTATATAAGC AGAGCTCGTT TAG                                     23
153 (2) INFORMATION FOR SEQ ID NO: 6:
155     (i) SEQUENCE CHARACTERISTICS:
156         (A) LENGTH: 30 base pairs
157         (B) TYPE: nucleic acid
158         (C) STRANDEDNESS: single
159         (D) TOPOLOGY: linear
161     (ii) MOLECULE TYPE: cDNA
162     (iii) HYPOTHETICAL: NO
C--> 163     (iv) ANTI-SENSE: YES
W--> 164     (v) FRAGMENT TYPE:
165         (vi) ORIGINAL SOURCE:
167     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
169 GTAGCAAAGA TCTAAGGACG GTGACTGCAG                               30
171 (2) INFORMATION FOR SEQ ID NO: 7:
173     (i) SEQUENCE CHARACTERISTICS:
174         (A) LENGTH: 39 base pairs
175         (B) TYPE: nucleic acid
176         (C) STRANDEDNESS: single
177         (D) TOPOLOGY: linear
179     (ii) MOLECULE TYPE: cDNA
180     (iii) HYPOTHETICAL: NO
C--> 181     (iv) ANTI-SENSE: NO
W--> 182     (v) FRAGMENT TYPE:
183         (vi) ORIGINAL SOURCE:
185     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
187 GTATGTGTCT GAAAATGAGC GTGGAGATTG GGCTCGCAC                     39
189 (2) INFORMATION FOR SEQ ID NO: 8:
191     (i) SEQUENCE CHARACTERISTICS:
192         (A) LENGTH: 39 base pairs
193         (B) TYPE: nucleic acid
194         (C) STRANDEDNESS: single
195         (D) TOPOLOGY: linear
197     (ii) MOLECULE TYPE: cDNA
198     (iii) HYPOTHETICAL: NO
C--> 199     (iv) ANTI-SENSE: YES
W--> 200     (v) FRAGMENT TYPE:

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Output Set: N:\CRF3\09142001\I835694.raw

201 (vi) ORIGINAL SOURCE:
 203 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 205 GTGCGAGCCC AATCTCCACG CTCATTTTCA GACACATAC 39
 207 (2) INFORMATION FOR SEQ ID NO: 9:
 209 (i) SEQUENCE CHARACTERISTICS:
 210 (A) LENGTH: 9 amino acids
 211 (B) TYPE: amino acid
 212 (C) STRANDEDNESS: single
 213 (D) TOPOLOGY: linear
 215 (ii) MOLECULE TYPE: peptide
 216 (iii) HYPOTHETICAL: NO
 C--> 217 (iv) ANTI-SENSE: NO
 W--> 218 (v) FRAGMENT TYPE: None
 219 (vi) ORIGINAL SOURCE:
 221 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 223 Thr Tyr Gln Arg Thr Arg Ala Leu Val
 224 1 5
 226 (2) INFORMATION FOR SEQ ID NO: 10:
 228 (i) SEQUENCE CHARACTERISTICS:
 229 (A) LENGTH: 4432 base pairs
 230 (B) TYPE: nucleic acid
 231 (C) STRANDEDNESS: double
 232 (D) TOPOLOGY: both
 234 (ii) MOLECULE TYPE: cDNA
 235 (iii) HYPOTHETICAL: NO
 C--> 236 (iv) ANTI-SENSE: NO
 W--> 237 (v) FRAGMENT TYPE:
 238 (vi) ORIGINAL SOURCE:
 240 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 242 TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA 60
 243 CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG TCAGCGGGTG 120
 244 TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC 180
 245 ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGATTGG 240
 246 CTATTGGCCA TTGCATACGT TGTATCCATA TCATAATATG TACATTTATA TTGGCTCATG 300
 247 TCCAACATTA CCGCCATGTT GACATTGATT ATTGACTAGT TATTAATAGT AATCAATTAC 360
 248 GGGGTCATTA GTTCATAGCC CATATATGGA GTTCCGCGTT ACATAACTTA CGGTAAATGG 420
 249 CCCGCCTGGC TGACCGCCCA ACGACCCCGG CCCATTGACG TCAATAATGA CGTATGTTCC 480
 250 CATAGTAACG CCAATAGGGA CTTTCCATTG ACGTCAATGG GTGGAGTATT TACGGTAAAC 540
 251 TGCCCACTTG GCAGTACATC AAGTGTATCA TATGCCAAGT ACGCCCCCTA TTGACGTCAA 600
 252 TGACGGTAAA TGGCCCGCCT GGCATTATGC CCAGTACATG ACCTTATGGG ACTTTCCTAC 660
 253 TTGGCAGTAC ATCTACGTAT TAGTCATCGC TATTACCATG GTGATGCGGT TTTGGCAGTA 720
 254 CATCAATGGG CGTGGATAGC GGTTTGAATC ACGGGGATTT CCAAGTCTCC ACCCCATTGA 780
 255 CGTCAATGGG AGTTTGTGTTT GGCACCAAAA TCAACGGGAC TTTCCAAAAT GTCGTAACAA 840
 256 CTCCGCCCCA TTGACGCAAA TGGGCGGTAG GCGTGTACGG TGGGAGGTCT ATATAAGCAG 900
 257 AGCTCGTTTA GTGAACCGTC AGATCGCCTG GAGACGCCAT CCACGCTGTT TTGACCTCCA 960
 258 TAGAAGACAC CGGGACCGAT CCAGCCTCCG CGGCCGGGAA CGGTGCATTG GAACGCGGAT 1020
 259 TCCCCGTGCC AAGAGTGACG TAAGTACCGC CTATAGAGTC TATAGGCCCA CCCCCTTGGC 1080
 260 TTCTTATGCA TGCTATACTG TTTTGGGCTT GGGGTCTATA CACCCCGCT TCCTCATGTT 1140
 261 ATAGGTGATG GTATAGCTTA GCCTATAGGT GTGGGTATT GACCATTATT GACCACTCCC 1200

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262	CTATTGGTGA	CGATACTTTC	CATTACTAAT	CCATAACATG	GCTCTTTGCC	ACAACTCTCT	1260
263	TTATTGGCTA	TATGCCAATA	CACTGTCTCT	CAGAGACTGA	CACGGACTCT	GTATTTTAC	1320
264	AGGATGGGGT	CTCATTTATT	ATTTACAAAT	TCACATATAC	AACACCACCG	TCCCCAGTGC	1380
265	CCGCAGTTT	TATTAAACAT	AACGTGGGAT	CTCCACGCGA	ATCTCGGGTA	CGTGTTCCGG	1440
266	ACATGGGCTC	TTCTCCGGTA	GCGGCGGAGC	TTCTACATCC	GAGCCCTGCT	CCCATGCCTC	1500
267	CAGCGACTCA	TGGTCGCTCG	GCAGCTCCTT	GCTCCTAACA	GTGGAGGCCA	GACTTAGGCA	1560
268	CAGCACGATG	CCCACCACCA	CCAGTGTGCC	GCACAAGGCC	GTGGCCGTAG	GGTATGTGTC	1620
269	TGAAAATGAG	CTCGGGGAGC	GGGCTTGCAC	CGCTGACGCA	TTTGGGAAGAC	TTAAGGCAGC	1680
270	GGCAGAAGAA	GATGCAGGCA	GCTGAGTTGT	TGTGTTCTGA	TAAGAGTCAG	AGGTAACCTC	1740
271	CGTTGCGGTG	CTGTTAACGG	TGGAGGGCAG	TGTAGTCTGA	GCAGTACTCG	TTGCTGCCGC	1800
272	GCGCGCCACC	AGACATAATA	GCTGACAGAC	TAACAGACTG	TTCTTTTCCA	TGGGCTTTT	1860
273	CTGCAGTCAC	CGTCTTAGA	TCTGCTGTGC	CTTCTAGTTG	CCAGCCATCT	GTTGTTTGCC	1920
274	CCTCCCCCGT	GCCTTCCTTG	ACCCTGGAAG	GTGCCACTCC	CACTGTCCTT	TCCTAATAAA	1980
275	ATGAGGAAAT	TGCATCGCAT	TGTCTGAGTA	GGTGTCAATC	TATTCTGGGG	GGTGGGGTGG	2040
276	GGCAGCACAG	CAAGGGGGAG	GATTGGGAAG	ACAATAGCAG	GCATGCTGGG	GATGCGGTGG	2100
277	GCTCTATGGG	TACCCAGGTG	CTGAAGAATT	GACCCGGTTC	CTCCTGGGCC	AGAAAGAAGC	2160
278	AGGCACATCC	CCTTCTCTGT	GACACACCCT	GTCCACGCCC	CTGGTTCTTA	GTTCCAGCCC	2220
279	CACTCATAGG	ACACTCATAG	CTCAGGAGGG	CTCCGCCTTC	AATCCCACCC	GCTAAAGTAC	2280
280	TTGGAGCGGT	CTCTCCCTCC	CTCATCAGCC	CACCAAACCA	AACCTAGCCT	CCAAGAGTGG	2340
281	GAAGAAATTA	AAGCAAGATA	GGCTATTAAG	TGCAGAGGGA	GAGAAAATGC	CTCCAACATG	2400
282	TGAGGAAGTA	ATGAGAGAAA	TCATAGAATT	TCTTCCGCTT	CCTCGCTCAC	TGACTCGCTG	2460
283	CGCTCGGTG	TTGGGCTGCG	GCGAGCGGTA	TCAGCTCACT	CAAAGGCGGT	AATACGGTTA	2520
284	TCCACAGAAT	CAGGGGATAA	CGCAGGAAAG	AACATGTGAG	CAAAAGGCCA	GCAAAAGGCC	2580
285	AGGAACCGTA	AAAAGGCCGC	GTTGCTGGCG	TTTTCCTATA	GGCTCCGCCC	CCCTGACGAG	2640
286	CATCACAAAA	ATCGACGCTC	AAGTCAGAGG	TGGCGAAACC	CGACAGGACT	ATAAAGATAC	2700
287	CAGGCGTTTC	CCCCTGGAAG	CTCCCTCGTG	CGCTCTCCTG	TTCCGACCCT	GCCGCTTACC	2760
288	GGATACCTGT	CCGCCTTTCT	CCCTTCGGGA	AGCGTGCGCG	TTTCTCAATG	CTCAGCTGTG	2820
289	AGGTATCTCA	GTTCCGGTGA	GGTCGTTTCG	TCCAAGCTGG	GCTGTGTGCA	CGAACCCCCC	2880
290	GTTTCAGCCG	ACCGCTGCGC	CTTATCCGGT	AACATCGTTC	TTGAGTCCAA	CCCGGTAAGA	2940
291	CACGACTTAT	CGCCACTGGC	AGCAGCCACT	GGTAACAGGA	TTAGCAGAGC	GAGGTATGTA	3000
292	GGCGGTGCTA	CAGAGTTCTT	GAAGTGGTGG	CCTAACTACG	GCTACACTAG	AAGGACAGTA	3060
293	TTTGGTATCT	GCGCTCTGCT	GAAGCCAGTT	ACCTTCGGAA	AAAGAGTTGG	TAGCTCTTGA	3120
294	TCCGGCAAAC	AAACCACCGC	TGGTAGCGGT	GGTTTTTTTG	TTTGCAAGCA	GCAGATTACG	3180
295	CGCAGAAAAA	AAGGATCTCA	AGAAGATCCT	TTGATCTTTT	CTACGGGGTC	TGACGCTCAG	3240
296	TGGAACGAAA	ACTCACGTTA	AGGGATTTTG	GTCATGAGAT	TATCAAAAAG	GATCTTCACC	3300
297	TAGATCCTTT	TAAATTAATA	ATGAAGTTTT	AAATCAATCT	AAAGTATATA	TGAGTAAACT	3360
298	TGGTCTGACA	GTTACCAATG	CTTAATCAGT	GAGGCACCTA	TCTCAGCGAT	CTGTCTATTT	3420
299	CGTTCATCCA	TAGTTGCCTG	ACTCCCCGTC	GTGTAGATAA	CTACGATACG	GGAGGGCTTA	3480
300	CCATCTGGCC	CCAGTGCTGC	AATGATAACG	CGAGACCCAC	GCTCACCAGC	TCCAGATTTA	3540
301	TCAGCAATAA	ACCAGCCAGC	CGGAAGGGCC	GAGCGCAGAA	GTGGTCCTGC	AACTTTATCC	3600
302	GCCTCCATCC	AGTCTATTAA	TTGTTGCCGG	GAAGCTAGAG	TAAGTAGTTC	GCCAGTTAAT	3660
303	AGTTTGCGCA	ACGTTGTTGC	CATTGCTACA	GGCATCGTGG	TGTCACGCTC	GTCGTTTGGT	3720
304	ATGGCTTCAT	TCAGCTCCGG	TTCCCAACGA	TCAAGGCGAG	TTACATGATC	CCCCATGTTG	3780
305	TGCAAAAAAG	CGGTTAGCTC	CTTCGGTCTT	CCGATCGTTG	TCAGAAGTAA	GTTGGCCGCA	3840
306	GTGTTATCAC	TCATGGTTAT	GGCAGCACTG	CATAATTCTC	TTACTGTTCAT	GCCATCCGTA	3900
307	AGATGCTTTT	CTGTGACTGG	TGAGTACTCA	ACCAAGTCAT	TCTGAGAATA	GTGTATGCGG	3960
308	CGACCGAGTT	GCTCTTGCCC	GGCGTCAATA	CGGGATAATA	CCGCGCCACA	TAGCAGAACT	4020
309	TTAAAAGTGC	TCATCATTGG	AAAACGTTCT	TCGGGGCGAA	AACTCTCAAG	GATCTTACCG	4080
310	CTGTTGAGAT	CCAGTTCGAT	GTAACCCACT	CGTGCACCCA	ACTGATCTTC	AGCATCTTTT	4140

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/835,694

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TIME: 11:06:24

Input Set : A:\18972PCA.txt

Output Set: N:\CRF3\09142001\I835694.raw

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:13 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:73 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:74 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=1
L:91 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:92 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=2
L:109 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:110 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=3
L:127 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:128 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=4
L:145 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:146 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=5
L:163 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:164 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=6
L:181 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:182 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=7
L:199 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:200 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=8
L:217 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:218 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=9
L:236 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:237 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=10
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L:328 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=11
L:381 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
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L:401 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=13
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L:598 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
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L:654 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:655 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=22

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L:672 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:673 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=23
L:690 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:691 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=24
L:708 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
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L:782 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=29
L:799 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:800 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=30
L:817 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:818 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=31
L:835 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:836 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=32
L:853 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:854 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=33
L:871 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:872 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=34
L:889 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:890 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=35
L:907 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:908 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=36
L:925 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:926 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=37
L:943 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:944 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=38
L:961 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:962 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=39
L:979 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:980 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=40
L:997 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:998 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=41
L:1015 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1016 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=42
L:1033 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1034 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=43
L:1051 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1052 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=44
L:1069 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1070 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=45
L:1146 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1147 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=46
L:1166 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=47

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/835,694

DATE: 09/14/2001

TIME: 11:06:24

Input Set : A:\18972PCA.txt

Output Set: N:\CRF3\09142001\I835694.raw

L:1185 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=48
L:1204 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=49
L:1223 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=50